

### REMARKS

Claims 1-45 stand cancelled and claims 46-56 are pending. Claim 46 has been amended herein. No new matter has been added by virtue of this amendment; support therefore being found throughout the specification and in the original and earlier presented claims of the application. In particular, support for the amended claim appears in the present application at page 5, lines 5-14, page 8, lines 8-15 and lines 21-24, page 14, lines 2-10, and page 20, lines 6-13.

The Office Action alleges that Applicants' response filed on July 2, 2003 was not fully responsive to the prior Office Action (paper no. 17). Applicants, therefore, offer the following remarks concerning the prior art rejections in a further effort to substantiate the arguments presented in their earlier filed response.

Claims 30, 32, 33 and 36 stand rejected under 35 USC §102(a) over Wilson et al. (*Biochemical and Biophysical Research Communications*, Vo. 232, pp. 678-681, 1997).

At the outset, Applicants note that each of the rejected claims has been cancelled and the subject matter thereof rewritten in newly presented method claims 46-54. In any event, the rejection is traversed.

Applicants submit that the cited reference does not teach or suggest the subject matter of claims 46-54 in any manner sufficient to sustain the §102(a) rejection. For example, see *In re Marshall*, 198 USPQ 344, 346 (CCPA 1978) ("[r]ejections under 35 U.S.C. §102 are proper only when the claimed subject matter is identically disclosed or described in the prior art.").

Wilson et al. does not teach *the method of making a nucleic acid* recited in the claims of the present application. For instance, independent claim 46 recites a method of making a nucleic acid having a modified base sequence of a gene for transforming a plant, comprising modifying a gene of another species by features (A) and (B) without altering the amino acid sequence thereof,

in order to avoid poly(A) addition. In accordance with the present invention, features (A) and (B) of Applicants' claimed method are defined as follows:

- (A) eliminating GT rich regions comprising 8 or more consecutive bases of G or T within the coding region of the gene, and
- (B) eliminating sequences encoded by AATAAA, NATAAA, ANTAAA, AANAAA, AATNAA, AATANA, or AATAAN within the coding region of the gene.

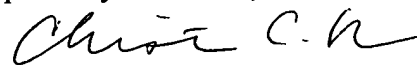
Applicants' method is clearly not taught or even suggested by the Wilson, et al. reference. Accordingly, the rejection is properly withdrawn.

Additionally, it is Applicants' understanding based on the Office Action of February 11, 2003, that the subject matter of former claims 31, 34, 35 and 37-45 was free of the prior art. The subject of those former claims is now reflected, in part, in present claims 55 and 56. In the event that the Wilson et al. reference were applied to the noted claims, Applicants submit the following traversal.

Wilson et al. clearly does not teach or suggest the subject matter of claims 55-56 in any manner sufficient to sustain a §102 or even §103 rejection. Clearly, it is a feature of claims 55-56 that the nucleic acid have a modified base sequence of a ferric-chelate reductase gene derived from *Saccharomyces cerevisiae* FRE1, which does not comprise the sequence disclosed by Wilson et al. Thus, any rejection of claims 55-56 in view of Wilson et al. should be withdrawn.

It is believed the application is in condition for immediate allowance, which action is earnestly solicited.

Respectfully submitted,



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